

SEQUENCE LISTING

<110> Microbiological Research Authority
Raven, Neil

<120> DEGRADATION AND DETECTION OF TSE INFECTIVITY

<130> GWS/22516

<150> GB 0104696.0

<151> 2001-02-26

<150> GB 0100420.9

<151> 2001-01-08

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 11

<212> PRT

<213> synthetic

<400> 1

Cys Gly Gly Trp Gly Gln Pro His Gly Gly Cys
1 5 10

<210> 2

<211> 23

<212> PRT

<213> synthetic

<400> 2

Cys Gly Gly Tyr Met Leu Gly Ser Ala Met Ser Arg Pro Ile Ile His
1 5 10 15

Phe Gly Asn Asp Tyr Glu Cys
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<210> 3

<211> 25

<212> PRT

<213> synthetic

<400> 3

Cys Val Asn Ile Thr Ile Lys Gln His Thr Val Thr Thr Thr Thr Lys
1 5 10 15

Gly Glu Asn Phe Thr Glu Thr Asp Cys
20 25

<210> 4

<211> 19

<212> PRT

<213> synthetic

<400> 4

Cys Ile Thr Gln Tyr Gln Arg Glu Ser Gln Ala Tyr Tyr Gln Arg Gly
1 5 10 15

Ala Ser Cys

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 6

<210> SEQ ID NO: 5

<211> LENGTH: 1497

<212> TYPE: DNA

<213> ORGANISM: B. amyloliquefaciens

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (96)...(1245)

<400> SEQUENCE: 5

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ttattctgca atgaaaaaa aggagaggat aaaga gtg aga ggc aaa aaa gta 113

Met Arg Gly Lys Lys Val

1

5

tgg atc agt ttg ctg ttt gct tta gcg tta atc ttt acg atg gcg ttc 161

Trp Ile Ser Leu Leu Phe Ala Leu Ala Leu Ile Phe Thr Met Ala Phe

10

15

20

ggc agc aca tcc tct gcc cag gcg gca ggg aaa tca aac ggg gaa aag 209

Gly Ser Thr Ser Ser Ala Gln Ala Ala Gly Lys Ser Asn Gly Glu Lys

25

30

35

aaa tat att gtc ggg ttt aaa cag aca atg agc acg atg agc gcc gct 257

Lys Tyr Ile Val Gly Phe Lys Gln Thr Met Ser Thr Met Ser Ala Ala

40

45

50

aag aag aaa gat gtc att tct gaa aaa ggc ggg aaa gtg caa aag caa 305

Lys Lys Lys Asp Val Ile Ser Glu Lys Gly Gly Lys Val Gln Lys Gln

55

60

65

70

ttc aaa tat gta gac gca gct tca gtc aca tta aac gaa aaa gct gta 353

Phe Lys Tyr Val Asp Ala Ala Ser Val Thr Leu Asn Glu Lys Ala Val

75

80

85

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aaa gaa ttg aaa aaa gac ccg agc gtc gct tac gtt gaa gaa gat cac Lys Glu Leu Lys Lys Asp Pro Ser Val Ala Tyr Val Glu Glu Asp His 90 95 100	401
gta gca cat gcg tac gcg cag tcc gtg cct tac ggc gta tca caa att Val Ala His Ala Tyr Ala Gln Ser Val Pro Tyr Gly Val Ser Gln Ile 105 110 115	449
aaa gcc cct gct ctg cac tct caa ggc tac act gga tca aat gtt aaa Lys Ala Pro Ala Leu His Ser Gln Gly Tyr Thr Gly Ser Asn Val Lys 120 125 130	497
gta gcg gtt atc gac agc ggt atc gat tct tct cat cct gat tta aag Val Ala Val Ile Asp Ser Gly Ile Asp Ser Ser His Pro Asp Leu Lys 135 140 145 150	545
gta gca agc gga gcc agc atg gtt cct tct gaa aca aat cct ttc caa Val Ala Ser Gly Ala Ser Met Val Pro Ser Glu Thr Asn Pro Phe Gln 155 160 165	593
gac aac aac tct cac gga act cac gtt gcc ggc aca gtt gcg gct ctt Asp Asn Asn Ser His Gly Thr His Val Ala Gly Thr Val Ala Ala Leu 170 175 180	641
aat aac tca atc ggt gta tta ggc gtt gcg cca agc gca tca ctt tac Asn Asn Ser Ile Gly Val Leu Gly Val Ala Pro Ser Ala Ser Leu Tyr 185 190 195	689
gct gta aaa gtt ctc ggt gct gac ggt tcc ggc caa tac agc tgg atc Ala Val Lys Val Leu Gly Ala Asp Gly Ser Gly Gln Tyr Ser Trp Ile 200 205 210	737
att aac gga atc gag tgg gcg atc gca aac aat atg gac gtt att aac Ile Asn Gly Ile Glu Trp Ala Ile Ala Asn Asn Met Asp Val Ile Asn 215 220 225 230	785
atg agc ctc ggc gga cct tct ggt tct gct gct tta aaa gcg gca gtt Met Ser Leu Gly Gly Pro Ser Gly Ser Ala Ala Leu Lys Ala Ala Val 235 240 245	833
gat aaa gcc gtt gca tcc ggc gtc gta gtc gtt gcg gca gcc ggt aac Asp Lys Ala Val Ala Ser Gly Val Val Val Val Ala Ala Gly Asn 250 255 260	881
gaa ggc act tcc ggc agc tca agc aca gtg ggc tac cct ggt aaa tac Glu Gly Thr Ser Gly Ser Ser Ser Thr Val Gly Tyr Pro Gly Lys Tyr 265 270 275	929
cct tct gtc att gca gta ggc gct gtt gac agc agc aac caa aga gca Pro Ser Val Ile Ala Val Gly Ala Val Asp Ser Ser Asn Gln Arg Ala 280 285 290	977
tct ttc tca agc gta gga cct gag ctt gat gtc atg gca cct ggc gta Ser Phe Ser Ser Val Gly Pro Glu Leu Asp Val Met Ala Pro Gly Val 295 300 305 310	1025
tct atc caa agc acg ctt cct gga aac aaa tac ggg gcg tac aac ggt Ser Ile Gln Ser Thr Leu Pro Gly Asn Lys Tyr Gly Ala Tyr Asn Gly 315 320 325	1073
acg tca atg gca tct ccg cac gtt gcc gga gcg gct gct ttg att ctt Thr Ser Met Ala Ser Pro His Val Ala Gly Ala Ala Leu Ile Leu 330 335 340	1121
tct aag cac ccg aac tgg aca aac act caa gtc cgc agc agt tta gaa Ser Lys His Pro Asn Trp Thr Asn Thr Gln Val Arg Ser Ser Leu Glu 345 350 355	1169
aac acc act aca aaa ctt ggt gat tct ttg tac tat gga aaa ggg ctg Asn Thr Thr Thr Lys Leu Gly Asp Ser Leu Tyr Tyr Gly Lys Gly Leu 360 365 370	1217
atc aac gta caa gcg gca gct cag taa a acataaaaaa ccggccttgg Ile Asn Val Gln Ala Ala Ala Gln 375 380	1265
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<210> SEQ ID NO: 6
 <211> LENGTH: 382
 <212> TYPE: PRT
 <213> ORGANISM: B. amyloliquefaciens

<400> SEQUENCE: 6

Met Arg Gly Lys Lys Val Trp Ile Ser Leu Leu Phe Ala Leu Ala Leu
 1 5 10 15
 Ile Phe Thr Met Ala Phe Gly Ser Thr Ser Ser Ala Gln Ala Ala Gly
 20 25 30
 Lys Ser Asn Gly Glu Lys Lys Tyr Ile Val Gly Phe Lys Gln Thr Met
 35 40 45
 Ser Thr Met Ser Ala Ala Lys Lys Lys Asp Val Ile Ser Glu Lys Gly
 50 55 60
 Gly Lys Val Gln Lys Gln Phe Lys Tyr Val Asp Ala Ala Ser Val Thr
 65 70 75 80
 Leu Asn Glu Lys Ala Val Lys Glu Leu Lys Lys Asp Pro Ser Val Ala
 85 90 95
 Tyr Val Glu Glu Asp His Val Ala His Ala Tyr Ala Gln Ser Val Pro
 100 105 110
 Tyr Gly Val Ser Gln Ile Lys Ala Pro Ala Leu His Ser Gln Gly Tyr
 115 120 125
 Thr Gly Ser Asn Val Lys Val Ala Val Ile Asp Ser Gly Ile Asp Ser
 130 135 140
 Ser His Pro Asp Leu Lys Val Ala Ser Gly Ala Ser Met Val Pro Ser
 145 150 155 160
 Glu Thr Asn Pro Phe Gln Asp Asn Asn Ser His Gly Thr His Val Ala
 165 170 175
 Gly Thr Val Ala Ala Leu Asn Asn Ser Ile Gly Val Leu Gly Val Ala
 180 185 190
 Pro Ser Ala Ser Leu Tyr Ala Val Lys Val Leu Gly Ala Asp Gly Ser
 195 200 205
 Gly Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu Trp Ala Ile Ala Asn
 210 215 220
 Asn Met Asp Val Ile Asn Met Ser Leu Gly Gly Pro Ser Gly Ser Ala
 225 230 235 240
 Ala Leu Lys Ala Ala Val Asp Lys Ala Val Ala Ser Gly Val Val Val
 245 250 255
 Val Ala Ala Ala Gly Asn Glu Gly Thr Ser Gly Ser Ser Ser Thr Val
 260 265 270
 Gly Tyr Pro Gly Lys Tyr Pro Ser Val Ile Ala Val Gly Ala Val Asp
 275 280 285
 Ser Ser Asn Gln Arg Ala Ser Phe Ser Ser Val Gly Pro Glu Leu Asp
 290 295 300
 Val Met Ala Pro Gly Val Ser Ile Gln Ser Thr Leu Pro Gly Asn Lys
 305 310 315 320
 Tyr Gly Ala Tyr Asn Gly Thr Ser Met Ala Ser Pro His Val Ala Gly
 325 330 335
 Ala Ala Ala Leu Ile Leu Ser Lys His Pro Asn Trp Thr Asn Thr Gln
 340 345 350

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Val Arg Ser Ser Leu Glu Asn Thr Thr Thr Lys Leu Gly Asp Ser Leu
 355 360 365
 Tyr Tyr Gly Lys Gly Leu Ile Asn Val Gln Ala Ala Gln
 370 375 380

<210> SEQ ID NO 7
 <211> LENGTH: 275
 <212> TYPE: PRT
 <213> ORGANISM: B. amyloliquefaciens

<400> SEQUENCE: 7

Ala Gln Ser Val Pro Tyr Gly Val Ser Gln Ile Lys Ala Pro Ala Leu
 1 5 10 15
 His Ser Gln Gly Tyr Thr Gly Ser Asn Val Lys Val Ala Val Ile Asp
 20 25 30
 Ser Gly Ile Asp Ser Ser His Pro Asp Leu Lys Val Ala Gly Gly Ala
 35 40 45
 Ser Met Val Pro Ser Glu Thr Asn Pro Phe Gln Asp Asn Asn Ser His
 50 55 60
 Gly Thr His Val Ala Gly Thr Val Ala Ala Leu Asn Asn Ser Ile Gly
 65 70 75 80
 Val Leu Gly Val Ala Pro Ser Ala Ser Leu Tyr Ala Val Lys Val Leu
 85 90 95
 Gly Ala Asp Gly Ser Gly Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu
 100 105 110
 Trp Ala Ile Ala Asn Asn Met Asp Val Ile Asn Met Ser Leu Gly Gly
 115 120 125
 Pro Ser Gly Ser Ala Ala Leu Lys Ala Ala Val Asp Lys Ala Val Ala
 130 135 140
 Ser Gly Val Val Val Val Ala Ala Ala Gly Asn Glu Gly Thr Ser Gly
 145 150 155 160
 Ser Ser Ser Thr Val Gly Tyr Pro Gly Lys Tyr Pro Ser Val Ile Ala
 165 170 175
 Val Gly Ala Val Asp Ser Ser Asn Gln Arg Ala Ser Phe Ser Ser Val
 180 185 190
 Gly Pro Glu Leu Asp Val Met Ala Pro Gly Val Ser Ile Gln Ser Thr
 195 200 205
 Leu Pro Gly Asn Lys Tyr Gly Ala Tyr Asn Gly Thr Ser Met Ala Ser
 210 215 220
 Pro His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys His Pro Asn
 225 230 235 240
 Trp Thr Asn Thr Gln Val Arg Ser Ser Leu Glu Asn Thr Thr Thr Lys
 245 250 255
 Leu Gly Asp Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn Val Gln Ala
 260 265 270
 Ala Ala Gln
 275

<210> SEQ ID NO 8
 <211> LENGTH: 275
 <212> TYPE: PRT
 <213> ORGANISM: B. subtilis

<400> SEQUENCE: 8

Ala Gln Ser Val Pro Tyr Gly Ile Ser Gln Ile Lys Ala Pro Ala Leu
 1 5 10 15

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His Ser Gln Gly Tyr Thr Gly Ser Asn Val Lys Val Ala Val Ile Asp
 20 25 30
 Ser Gly Ile Asp Ser Ser His Pro Asp Leu Asn Val Arg Gly Gly Ala
 35 40 45
 Ser Phe Val Pro Ser Glu Thr Asn Pro Tyr Gln Asp Gly Ser Ser His
 50 55 60
 Gly Thr His Val Ala Gly Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly
 65 70 75 80
 Val Leu Gly Val Ser Pro Ser Ala Ser Leu Tyr Ala Val Lys Val Leu
 85 90 95
 Asp Ser Thr Gly Ser Gly Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu
 100 105 110
 Trp Ala Ile Ser Asn Asn Met Asp Val Ile Asn Met Ser Leu Gly Gly
 115 120 125
 Pro Thr Gly Ser Thr Ala Leu Lys Thr Val Val Asp Lys Ala Val Ser
 130 135 140
 Ser Gly Ile Val Val Ala Ala Ala Ala Gly Asn Glu Gly Ser Ser Gly
 145 150 155 160
 Ser Thr Ser Thr Val Gly Tyr Pro Ala Lys Tyr Pro Ser Thr Ile Ala
 165 170 175
 Val Gly Ala Val Asn Ser Ser Asn Gln Arg Ala Ser Phe Ser Ser Ala
 180 185 190
 Gly Ser Glu Leu Asp Val Met Ala Pro Gly Val Ser Ile Gln Ser Thr
 195 200 205
 Leu Pro Gly Gly Thr Tyr Gly Ala Tyr Asn Gly Thr Ser Met Ala Thr
 210 215 220
 Pro His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys His Pro Thr
 225 230 235 240
 Trp Thr Asn Ala Gln Val Arg Asp Arg Leu Glu Ser Thr Ala Thr Tyr
 245 250 255
 Leu Gly Asn Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn Val Gln Ala
 260 265 270
 Ala Ala Gln
 275

<210> SEQ ID NO: 9
 <211> LENGTH: 274
 <212> TYPE: PRT
 <213> ORGANISM: B. licheniformis

<400> SEQUENCE: 9

Ala Gln Thr Val Pro Tyr Gly Ile Pro Leu Ile Lys Ala Asp Lys Val
 1 5 10 15
 Gln Ala Gln Gly Phe Lys Gly Ala Asn Val Lys Val Ala Val Leu Asp
 20 25 30
 Thr Gly Ile Gln Ala Ser His Pro Asp Leu Asn Val Val Gly Gly Ala
 35 40 45
 Ser Phe Val Ala Gly Glu Ala Tyr Asn Thr Asp Gly Asn Gly His Gly
 50 55 60
 Thr His Val Ala Gly Thr Val Ala Ala Leu Asp Asn Thr Thr Gly Val
 65 70 75 80
 Leu Gly Val Ala Pro Ser Val Ser Leu Tyr Ala Val Lys Val Leu Asn
 85 90 95
 Ser Ser Gly Ser Gly Ser Tyr Ser Gly Ile Val Ser ly Ile Glu Trp

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100	105	110
Ala Thr Thr Asn Gly Met Asp Val	Ile Asn Met Ser Leu Gly Gly Ala	
115	120	125
Ser Gly Ser Thr Ala Met Lys Gln Ala Val Asp Asn Ala Tyr Ala Arg		
130	135	140
Gly Val Val Val Val Ala Ala Ala Gly Asn Ser Gly Asn Ser Gly Ser		
145	150	155
Thr Asn Thr Ile Gly Tyr Pro Ala Lys Tyr Asp Ser Val Ile Ala Val		
165	170	175
Gly Ala Val Asp Ser Asn Ser Asn Arg Ala Ser Phe Ser Ser Val Gly		
180	185	190
Ala Glu Leu Glu Val Met Ala Pro Gly Ala Gly Val Tyr Ser Thr Tyr		
195	200	205
Pro Thr Asn Thr Tyr Ala Thr Leu Asn Gly Thr Ser Met Ala Ser Pro		
210	215	220
His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys His Pro Asn Leu		
225	230	235
Ser Ala Ser Gln Val Arg Asn Arg Leu Ser Ser Thr Ala Thr Tyr Leu		
245	250	255
Gly Ser Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn Val Glu Ala Ala		
260	265	270
Ala Gln		

<210> SEQ ID NO 10
 <211> LENGTH: 269
 <212> TYPE: PRT
 <213> ORGANISM: B. lentus

<400> SEQUENCE: 10

Ala Gln Ser Val Pro Trp Gly Ile Ser Arg Val Gln Ala Pro Ala Ala		
1	5	10
His Asn Arg Gly Leu Thr Gly Ser Gly Val Lys Val Ala Val Leu Asp		
20	25	30
Thr Gly Ile Ser Thr His Pro Asp Leu Asn Ile Arg Gly Gly Ala Ser		
35	40	45
Phe Val Pro Gly Glu Pro Ser Thr Gln Asp Gly Asn Gly His Gly Thr		
50	55	60
His Val Ala Gly Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Leu		
65	70	75
Gly Val Ala Pro Ser Ala Glu Leu Tyr Ala Val Lys Val Leu Gly Ala		
85	90	95
Ser Gly Ser Gly Ser Val Ser Ser Ile Ala Gln Gly Leu Glu Trp Ala		
100	105	110
Gly Asn Asn Gly Met His Val Ala Asn Leu Ser Leu Gly Ser Pro Ser		
115	120	125
Pro Ser Ala Thr Leu Glu Gln Ala Val Asn Ser Ala Thr Ser Arg Gly		
130	135	140
Val Leu Val Val Ala Ala Ser Gly Asn Ser Gly Ala Gly Ser Ile Ser		
145	150	155
Tyr Pro Ala Arg Tyr Ala Asn Ala Met Ala Val Gly Ala Thr Asp Gln		
165	170	175
Asn Asn Asn Arg Ala Ser Phe Ser In Tyr Gly Ala ly Leu Asp Ile		
180	185	190
Val Ala Pro Gly Val Asn Val Gln Ser Thr Tyr Pro ly Ser Thr Tyr		

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195	200	205
Ala Ser Leu Asn Gly Thr	Ser Met Ala Thr	Pro His Val Ala Gly Ala
210	215	220
Ala Ala Leu Val Lys Gln	Lys Asn Pro Ser Trp	Ser Asn Val Gln Ile
225	230	235 240
Arg Asn His Leu Lys Asn	Thr Ala Thr Ser Leu	Gly Ser Thr Asn Leu
245	250	255
Tyr Gly Ser Gly Leu Val	Asn Ala Glu Ala Ala	Thr Arg
260	265	

SEQUENCE CHARACTERISTICS: Sequence variant MC3 of subtilisin from
Bacillus subtilis with amino acid mutations N76D, Q103A and Y104I (shown in bold
type)

SEQ ID NO ~~54~~ 11

LENGTH: 275

TYPE: PRT

ORGANISM: *B. subtilis*

~~SEQUENCE: 6~~

Ala	Gln	Ser	Val	Pro	Tyr	Gly	Ile	Ser	Gln	Ile	Lys	Ala	Pro	Ala	Leu	1	5	10	15
His	Ser	Gln	Gly	Tyr	Thr	Gly	Ser	Asn	Val	Lys	Val	Ala	Val	Ile	Asp	20	25	30	
Ser	Gly	Ile	Asp	Ser	Ser	His	Pro	Asp	Leu	Asn	Val	Arg	Gly	Gly	Ala	35	40	45	
Ser	Phe	Val	Pro	Ser	Glu	Thr	Asn	Pro	Tyr	Gln	Asp	Gly	Ser	Ser	His	50	55	60	
Gly	Thr	His	Val	Ala	Gly	Thr	Ile	Ala	Ala	Leu	Asp	Asn	Ser	Ile	Gly	65	70	75	80
Val	Leu	Gly	Val	Ser	Pro	Ser	Ala	Ser	Leu	Tyr	Ala	Val	Lys	Val	Leu	85	90	95	
Asp	Ser	Thr	Gly	Ser	Gly	Ala	Ile	Ser	Trp	Ile	Ile	Asn	Gly	Ile	Glu	100	105	110	
Trp	Ala	Ile	Ser	Asn	Asn	Met	Asp	Val	Ile	Asn	Met	Ser	Leu	Gly	Gly	115	120	125	
Pro	Thr	Gly	Ser	Thr	Ala	Leu	Lys	Thr	Val	Val	Asp	Lys	Ala	Val	Ser	130	135	140	
Ser	Gly	Ile	Val	Val	Ala	Ala	Ala	Gly	Asn	Glu	Gly	Ser	Ser	Gly		145	150	155	160
Ser	Thr	Ser	Thr	Val	Gly	Tyr	Pro	Ala	Lys	Tyr	Pro	Ser	Thr	Ile	Ala	165	170	175	
Val	Gly	Ala	Val	Asn	Ser	Ser	Asn	Gln	Arg	Ala	Ser	Phe	Ser	Ser	Ala	180	185	190	
Gly	Ser	Glu	Leu	Asp	Val	Met	Ala	Pro	Gly	Val	Ser	Ile	Gln	Ser	Thr	195	200	205	
Leu	Pro	Gly	Gly	Thr	Tyr	Gly	Ala	Tyr	Asn	Gly	Thr	Ser	Met	Ala	Thr	210	215	220	
Pro	His	Val	Ala	Gly	Ala	Ala	Ala	Leu	Ile	Leu	Ser	Lys	His	Pro	Thr	225	230	235	240
Trp	Thr	Asn	Ala	Gln	Val	Arg	Asp	Arg	Leu	Glu	Ser	Thr	Ala	Thr	Tyr	245	250	255	
Leu	Gly	Asn	Ser	Phe	Tyr	Tyr	Gly	Lys	Gly	Leu	Ile	Asn	Val	Gln	Ala	260	265	270	
Ala	Ala	Gln														275			

SEQUENCE CHARACTERISTICS: Sequence variant of subtilisin from *Bacillus lentus* with amino acid mutations N74D, S101A and V102I (shown in bold type)

SEQ ID NO ~~7~~ 12

LENGTH: 269

TYPE: PRT

ORGANISM: *B. lentus*

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Ala Gln Ser Val Pro Trp Gly Ile Ser Arg Val Gln Ala Pro Ala Ala
 1           5           10           15
His Asn Arg Gly Leu Thr Gly Ser Gly Val Lys Val Ala Val Leu Asp
 20           25           30
Thr Gly Ile Ser Thr His Pro Asp Leu Asn Ile Arg Gly Gly Ala Ser
 35           40           45
Phe Val Pro Gly Glu Pro Ser Thr Gln Asp Gly Asn Gly His Gly Thr
 50           55           60
His Val Ala Gly Thr Ile Ala Ala Leu Asp Asn Ser Ile Gly Val Leu
 65           70           75           80
Gly Val Ala Pro Ser Ala Glu Leu Tyr Ala Val Lys Val Leu Gly Ala
 85           90           95
Ser Gly Ser Gly Ala Ile Ser Ser Ile Ala Gln Gly Leu Glu Trp Ala
100           105           110
Gly Asn Asn Gly Met His Val Ala Asn Leu Ser Leu Gly Ser Pro Ser
115           120           125
Pro Ser Ala Thr Leu Glu Gln Ala Val Asn Ser Ala Thr Ser Arg Gly
130           135           140
Val Leu Val Val Ala Ala Ser Gly Asn Ser Gly Ala Gly Ser Ile Ser
145           150           155           160
Tyr Pro Ala Arg Tyr Ala Asn Ala Met Ala Val Gly Ala Thr Asp Gln
165           170           175
Asn Asn Asn Arg Ala Ser Phe Ser Gln Tyr Gly Ala Gly Leu Asp Ile
180           185           190
Val Ala Pro Gly Val Asn Val Gln Ser Thr Tyr Pro Gly Ser Thr Tyr
195           200           205
Ala Ser Leu Asn Gly Thr Ser Met Ala Thr Pro His Val Ala Gly Ala
210           215           220
Ala Ala Leu Val Lys Gln Lys Asn Pro Ser Trp Ser Asn Val Gln Ile
225           230           235           240
Arg Asn His Leu Lys Asn Thr Ala Thr Ser Leu Gly Ser Thr Asn Leu
245           250           255
Tyr Gly Ser Gly Leu Val Asn Ala Glu Ala Ala Thr Arg
260           265

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